THAT WHICH IS CLAIMED:

1. A method for altering a plant agronomic trait selected from the group consisting of time to flowering, duration of flowering in a plant, fruit yield, seed yield, root biomass, seed size, seed shape, number of stem branches, and size of a plant, the method comprising:

(a) introducing into a plant cell an expression cassette comprising a nucleotide sequence operably linked to a promoter that is operable within the plant cell, wherein the nucleotide sequence is selected from the group consisting of:

(*i*) a nucleotide sequence antisense to a plant *AGB1* or an *AGB1* ortholog,

(*ii*) a nucleotide sequence comprising an inverted repeat of *AGB1* or an *AGB1* ortholog,

(*iii*) a nucleotide sequence encoding a dsRNA, the dsRNA comprising a first RNA complementary to at least 25 consecutive nucleotides of a plant *AGB1* or an *AGB1* ortholog and a second RNA substantially complementary to the first RNA,

(*iv*) a nucleotide sequence that is *AGB1* or an *AGB1* ortholog, and

(*v*) a nucleotide sequence that is *GPA1* or a *GPA1* ortholog; and

(b) regenerating a plant that has a stably integrated expression cassette from the plant cell, wherein the regenerated plant has an altered agronomic trait.

2. The method of claim 1, wherein the promoter is selected from the group consisting of constitutive, inducible, developmentally regulated, tissue-preferred, minimal and 35S promoters.

3. The method of claim 1, wherein the plant is a dicot, a monocot, a gymnosperm or a member of the genus *Brassica*.

4. The method of claim 1, wherein the nucleotide sequence that is *AGB1* has the sequence set forth in SEQ ID NO:1.

5. The method of claim 1, wherein the nucleotide sequence that is *GPA1* has the sequence set forth in SEQ ID NO:3

6. The method of Claim 1, wherein the altered plant agronomic trait is time to flowering, and the regenerated plant has an altered time to flowering.

7. The method of Claim 1, wherein the altered plant agronomic trait is duration to flowering wherein the plant has an altered duration of flowering.

8. The method of Claim 1, wherein the altered plant agronomic trait is fruit yield, and the regenerated plant has an altered fruit yield.

9. The method of Claim 1, wherein the altered plant agronomic trait is seed yield, and the regenerated plant has an altered seed yield.

10. The method of Claim 1, wherein the altered plant agronomic trait is altered seed size and the regenerated plant has an altered seed size

11. The method of Claim 1, wherein the altered plant agronomic trait is seed shape and the regenerated plant has an altered seed shape.

12. The method of Claim 1, wherein the altered plant agronomic trait is altered plant size, and the regenerated plant has an altered plant size.

13. The method of Claim 1, wherein the altered plant agronomic trait is number of stem branches and the regenerated plant has an altered number of stem branches.

14. A method for altering a plant agronomic trait selected from the group consisting of time to flowering, duration of flowering in a plant, fruit yield, seed yield, root biomass, seed size, seed shape, number of stem branches, and size of a plant, the method comprising:

a) causing a disruption in a gene in a plant cell other than *Arabidopsis*, wherein the gene is an *AGB1* ortholog endogenous to the plant cell; and

b) regenerating a plant from the plant cell, wherein the plant has a disruption in the endogenous gene and the plant exhibits an altered agronomic trait.

15. The method of Claim 14, wherein the disruption is caused by a ribozyme complementary to the *AGB1* ortholog.

16. The method of Claim 14, wherein the disruption is caused by transposon or T-DNA insertion.

17. The method of Claim 14, wherein the disruption is caused by site-directed mutagenesis.

18. The method of Claim 14, wherein the disruption is caused by random mutagenesis.

19. A method for altering a plant agronomic trait selected from the group consisting of time to flowering, duration of flowering in a plant, fruit yield, seed yield, root biomass, seed size, seed shape, number of stem branches, and size of a plant, the method comprising:

a) causing a disruption in a gene in a plant cell that is not *Arabidopsis thaliana* or *Orzya sativa*, wherein the gene is a *GPA1* ortholog endogenous to the plant cell; and

b) regenerating a plant from the plant cell, wherein the plant has a disruption in the endogenous gene and the plant exhibits an altered fruit and seed yield.

20. The method of Claim 19, wherein the disruption is caused by a ribozyme complementary to the *GPA1* ortholog.

21. The method of Claim 19, wherein the disruption is caused by transposon or T-DNA insertion.

22. The method of Claim 19, wherein the disruption is caused by site-directed mutagenesis.

23. The method of Claim 19, wherein the disruption is caused by random mutagenesis.

24. A transgenic plant having stably integrated into its genome an expression cassette comprising a nucleotide sequence operably linked to a promoter that is operable within the plant, wherein the nucleotide sequence is selected from the group consisting of:

(a) a nucleotide sequence antisense to a nucleotide sequence that is *AGB1* or an *AGB1* ortholog,

(b) a nucleotide sequence comprising an inverted repeat of *AGB1* or an *AGB1* ortholog,

(c) a nucleotide sequence encoding a dsRNA, the dsRNA comprising a first RNA complementary to at least 25 consecutive nucleotides of a plant *AGB1* or an *AGB1* ortholog and a second RNA substantially complementary to the first RNA, and

(d) a nucleotide sequence that is *AGB1* or an *AGB1* ortholog.

25. The transgenic plant of claim 24, wherein the plant is a dicot, a monocot, a gymnosperm, a member of the genus *Brassica*, or *Brassica napus*.

26. Transgenic seed from the plant of claim 24.

27. A transgenic plant that is not *Arabidopsis*, wherein the plant has a disruption in a gene that is an *AGB1* ortholog endogenous to the plant.

28. The transgenic plant of claim 27, wherein the plant is a dicot, a monocot, a gymnosperm, a member of the genus *Brassica*, or *Brassica napus*.

29. A transgenic plant having stably integrated into its genome an expression cassette comprising a nucleotide sequence operably linked to a promoter that is operable within the plant, wherein the nucleotide sequence is selected from the group consisting of::

i) a nucleotide sequence antisense to a nucleotide sequence that is *GPA1* or a *GPA1* ortholog,

ii) a nucleotide sequence comprising an inverted repeat of *GPA1* or an *GPA1* ortholog,

iii) a nucleotide sequence encoding a dsRNA, the dsRNA comprising a first RNA complementary to at least 25 consecutive nucleotides of a plant *GPA1* or an *GPA1* ortholog and a second RNA substantially complementary to the first RNA, and

iv) a nucleotide sequence that is *GPA1* or a *GPA1* ortholog.

30. The transgenic plant of claim 29, wherein the plant is a dicot, a monocot, a member of the genus *Brassica*, or *Brassica napus*.

31. Transgenic seed from the plant of claim 29.

32. A transgenic plant that is not *Arabidopsis thaliana* or *Orzya sativa*, wherein the plant has a disruption in a gene that is a *GPA1* ortholog endogenous to the plant.

33. The transgenic plant of claim 32, wherein the plant is a dicot, a monocot, a member of the genus *Brassica*, or *Brassica napus*.

34. Transgenic seed from the plant of claim 32.

35. A method for producing a transgenic plant having increased root biomass, comprising:

generating a transgenic plant comprising a driver cassette comprising

(a) a synthetic chimeric transcription factor open reading frame operably linked to a root-preferred promoter; and

(b) a target cassette comprising a nucleotide sequence in the antisense orientation operably linked to a minimal promoter operably linked to at least one cognate upstream activating sequence, wherein the nucleotide sequence in the antisense orientation is selected from the group consisting of *(i)* at least a portion of an *AGB1* gene sequence set forth in SEQ ID NO:1 and *(ii)* at least a portion of an ortholog of an *AGB1* gene sequence set forth in SEQ ID NO:1;

wherein each of the driver and the target cassettes is stably integrated in the genome of the plant and the plant has an increased root biomass.

36. The method according to claim 35, wherein the root-preferred promoter is a bZIP root-preferred promoter

37. The method according to claim 35, wherein the root-preferred promoter is a D5 bZIP promoter

38. The method according to claim 35, wherein the synthetic chimeric transcription factor open reading frame is a GAL4/VP16 open reading frame.

39. The method according to claim 35, wherein driver cassette comprises a GAL4/VP16 open reading frame is operably linked to a bZIP root-preferred promoter.

40. The method according to claim 35, wherein at least one cognate upstream activating sequence is a GAL4 upstream activating sequence.

41. The method of claim 35, wherein the plant is selected from the group consisting of monocots, dicots, vegetable crops, tomato, potato, pea, spinach, tobacco, soybean, sunflower, peanut, alfalfa, mint, cotton, rice, maize, oats, wheat, barley, sorghum, grasses, *Brassica, Brassica napus*, and *Arabidopsis*.

42. A transgenic plant having increased root biomass, the plant comprising:

a) a driver cassette comprising a synthetic chimeric transcription factor open reading frame operably linked to a root-preferred promoter; and

b) a target cassette comprising a nucleotide sequence in the antisense orientation operably linked to a minimal promoter operably linked to at least one cognate upstream activating sequence;

wherein the nucleotide sequence is selected from the group consisting of: (*i*) at least a portion of an *AGB1* gene sequence set forth in SEQ ID NO:1 and (*ii*) at least a portion of an ortholog of an *AGB1* gene sequence set forth in SEQ ID NO:1; and

wherein the driver cassette and target cassette are stably integrated into the plant genome.

43. The transgenic plant of Claim 42, wherein the synthetic chimeric transcription factor open reading frame is a GAL4/VP16 open reading frame.

44. The transgenic plant of Claim 42, wherein the root-preferred promoter is bZIP root-preferred promoter

45. The transgenic plant of Claim 42, wherein the root-preferred promoter is a D5 bZIP promoter

46. The transgenic plant of Claim 42, wherein at least one cognate upstream activating sequence is a GAL4 upstream activating sequence.

47. The transgenic plant of Claim 42, wherein the driver cassette comprising a GAL4/VP16 open reading frame is operably linked to a D5 bZIP promoter.

48. The transgenic plant of claim 42, wherein the target cassette comprising at least a portion of an *AGB1* gene sequence set forth in SEQ ID NO:1 in the antisense orientation is operably linked to a minimal promoter operably linked to at least one GAL4 upstream activating sequence.

49. The transgenic plant of claim 42, wherein the plant is selected from the group consisting of monocots, dicots, vegetable crops, tomato, potato, pea, spinach, tobacco, soybean, sunflower, peanut, alfalfa, mint, cotton, rice, maize, oats, wheat, barley, sorghum, grasses, *Brassica, Brassica napus*, and *Arabidopsis*.

50. Transgenic seed of the plant of claim 42.